

Amendments to the Specification:

Please replace the paragraph starting on page 8, line 21 – page 9, line 7, with the following:

Figure 2: Structure and domains of the NFR5 protein. **a.** Schematic representation of the NFR5 protein domains. **b.** The amino acid sequence of NFR5 arranged in protein domains. Bold, conserved LysM residues. Bold and underlined residues conserved in protein kinase domains (KD); TM: transmembrane, SP: signal peptide. The asterisk indicates a stop codon in the *nfr5-3*; the black triangle a retrotransposon insertion in *nfr5-2* and the grey box defines the amino acids deleted in *nfr5-1*. **c.** Individual alignment of the three LysM motifs (M1, M2, M3) from NFR5, pea SYM10, *Medicago truncatula* (*M.t.*, Ac126779) rice (Ac103891), the single LysM in chitinase from *Volvox carteri* (Acc. No: T08150) and the pfam consensus. **d.** The divergent or absent activation loop (domain VIII) in the NFR5 family of receptor kinases is illustrated by alignment of kinase motifs VII, VIII and IX from *Arabidopsis* (At2g33580) NFR5, SYM10, *Medicago truncatula* (*M.t.*, Ac126779), rice (Ac103891) and the SMART consensus. Conserved domain VII aspartic acid is marked in bold and underlined. In Figures 2c and d, the amino acids conserved in all aligned motifs are marked in black bold and amino acids conserved in two or more motifs are marked in grey underlined.

Please replace the paragraph starting on page 9, line 22 – page 10, line 8, with the following:

Figure 5. Positional cloning of the *NFR1* gene. **a.** Genetic map of the region surrounding the *NFR1* locus. Positions of the closest AFLP, microsatellite- and PCR-markers are given together with genetic distances in cM. **b.** Physical map of the *NFR1* locus. BAC clones 56L2, 16K18, 10M24, 36D15, 56K22 and TAC clones LjT05B16, LjT02D13, LjT21I002, which cover the region are shown. The numbers of recombination events detected with BAC

and TAC end-markers or internal markers are given. Arrows indicate the positions of the two markers (10M24-2, 56L2-2) delimiting the *NFR1* locus. UFD and HP correspond to the UFD1-like protein and the hypothetical protein encoded in the region. c. Exon-intron structure of the *NFR1* gene. Boxes correspond to exons, where LysM motifs are shown in light-grey stippled boxes, trans-membrane region in black, kinase domains in dark-grey hatched boxes. Dotted lines define introns and full lines define the 5' and 3' un-translated regions. The nucleotide length of all exons and introns are indicated. The numbers between brackets correspond to exon and intron 4, corresponding to alternative splicing.